Free Paper Presentation 9: HBV & ESLD

Sunday, July 18, 2010, 07:30–08:30
Convention Hall 2A

PL-009 Combination of telbivudine and adefovir dipivoxil therapy in chronic hepatitis B patients with poor response to adefovir dipivoxil monotherapy

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Objectives: At present, there is no consensus of telbivudine (LdT) treatment for chronic hepatitis B (CHB) patients who have poor response to adevofir dipivoxil (ADV) monotherapy. The aim of this study was to assess the therapeutic effectiveness of LdT, administered in combination with ADV in CHB patients with poor response to ADV monotherapy.
Methods: Twenty-four adult outpatients aged >18 years with HBV DNA $\geqslant 10^3$ copies/mL and normal alanine aminotransferase (ALT) after at least 48 weeks of ADV initial monotherapy were included and immediately received ADV plus LdT combination treatment in this prospective study. HBV DNA and ALT levels were checked every 3 month. The proportions of patients who achieved virologic response (VR, undetectable HBV-DNA [$<10^3$ copies/mL]) were analyzed, and serum creatine kinase (CK) and creatinine (Cr) after combination therapy were observed.
Results: At baseline of combination treatment, the mean level of HBV DNA was 4.05 log (10) copies/mL. Compared with baseline, the mean decrease in HBV DNA level at week 12 and 24 were $-0.89\ \log_{10}$ and $-1.31\ \log_{10}$ copies/mL, respectively, and the decreasing was significant ($p < 0.001$for week 12, and $p < 0.001$ for week 24). The VR rate was 41.7% and 66.7% at weeks 12 and 24, respectively, and the difference in VR between week 12 and 24 was significant ($p = 0.003$). During the initial 24 weeks combination therapy, no elevated ALT, CK, and Cr were detected.
Conclusions: Adding LdT may be a good choice for CHB patients with poor response to ADV monotherapy. And further long-term study was necessary to confirm the results.

OL-041 Current distribution of HBV serological markers in chronic HBV patients and its significance in Mongolia

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Background: HBsAg seropositivity rate in healthy Mongolian population is about 10%. Although the prevalence for the virus infection has been confirmed in many other studies, the extended investigation for other viral markers was not reported before.
Method: Total of 1,961 patients were assessed for five HBV seromarkers HBsAg, HBeAb, HBsAb, and HBeAb, YBcAb during January 2009 and October 2009. HBV combo test was purchased from ACON Laboratories, Inc, USA. CBC was done using Sysmex, XS800i hematology analyzer, Japan, Statistical analysis was performed Microsoft Excel software. Out of 1,961 patients 381 were positive for HBsAg.
Result: In this single center study, we analyzed all patients (n = 381) positive for HBsAg. HBV infected males represented 53.2% (n = 203) of the total, with females representing 46.8% (n = 178). Only 3.6% of HBsAg positive patients were positive for HBeAg, with equal sex proportions. HBeAb+ patients comprise 19.9% (n = 76), out of which 77.6% (n+59) were positive for both HBcAb and HBeAb. Patients with HBcAb comprise 39.3% (n = 150) of the pool, with males representing 59.4% (n = 89). 203 patients (53.2%) were only positive for HBsAg, with no any antibodies present. We also checked platelet numbers for clues of liver cirrhosis. According to our study 8.8% (n = 8) of the patients who had full CBC (n = 90) were cirrhotic. All of those patients had albumin level <3.4 g/dL. Patient with double infection for both HCV (anti-HCV) and HBV (HBsAg) made 3.6% (n = 14) of the pool.
Conclusion: Cirrhotic patients may comprise nearly 9% of HBV infected patients, which will make around 24,000 patients (0.8% of the country population). Patients with bearing both HBV and HCV have higher risk of developing liver cirrhosis 7.1% vs. 1.9% consistent with the data of other countries. HBeAg positivity rate was very low 3.7%, which is much lower than of western nations.

OL-042 A quantitative analysis method for detecting the ratio of HBV mutant/wild strains

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Objectives: The purpose of this study was to develop a quantitative analysis method for detecting the ratio of HBV mutant/wild strains, which is standardized, direct and precise.
Methods: We designed a sequence map analysis software could calculate the relative proportions of mutant and wild strains. Bi-directional sequencing was used to improve the accuracy. Totally 62 Sera samples were collected from patients with hepatitis B who were predicted to develop viral breakthrough during lamivudine treatment at infectious department of NanFang Hospital, between 2008 and 2009. For samples with YMDD mutantion detected by PCR restriction-fragment-length-polymorphism (PCR-RFLP) assay firstly, we sequenced them bi-directional. After analysed the sequence maps by Chromas and DNAMAN and picked out the maps with double peaks at YMDD sites, we calculated the ratio of HBV mutant/wild strains.
Results: YMDD mutations were detected in 54 cases (54/62) by PCR-RFLP assay. The results of Bi-directional sequencing: 22 cases were YMDD mutation completely while 32 cases were found to coexist with wild-type virus. Among these cases, YVDD/YMDD, YIDD/YMDD and L180M mutation coexist with wild-type virus were 8, 6 and 27 cases, respectively. YVDD/YMDD or YIDD/YMDD accompanied by L180M mutation were 14 cases. Of all mixed infections cases, the smallest ratio of mutant strain is 5.68%, and the maximum ratio is 93.82%.
Conclusions: We developed a quantitative analysis method for detecting the ratio of HBV mutant/wild strains, which is standardized, direct and precise. For further study, it could be used to detect resistance of other nucleotides (acid) analogues dynamically. Also we could use this method to monitor a wide range of drug resistance loci simultaneously, and find new meaningful joint resistance mutation. This method could provide information to make a more reasonable prevention, diagnosis and treatment of HBV infection.